

# SEQUENCE LISTING

<110> Thompson, John E.  
Wang, Tzann-Wei  
Lu, Dongen Lilly

<120> DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC  
PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL  
DEATH IN PLANTS

<130> 10799/9

<140>

<141>

<150> 09/348,675

<151> 1999-07-06

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

<211> 1609

<212> DNA

<213> Lycopersicon sp.

<220>

<221> CDS

<222> (54..1196)

<220>

<223> DHS

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Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
          5              10              15

ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc      152
Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
          20              25              30

tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg      200
Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
          35              40              45

gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att      248
Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
          50              55              60              65

gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag      296
Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
          70              75              80

gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc      344
Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr
          85              90              95

tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt      392
Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val

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Val	Thr	Thr	Ala	Gly	Gly	Ile	Glu	Glu	Asp	Leu	Ile	Lys	Cys	Leu	Ala	
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Pro	Thr	Tyr	Lys	Gly	Asp	Phe	Ser	Leu	Pro	Gly	Ala	Ser	Leu	Arg	Ser	
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Lys	Gly	Leu	Asn	Arg	Ile	Gly	Asn	Leu	Leu	Val	Pro	Asn	Asp	Asn	Tyr	
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Cys	Lys	Phe	Glu	Asn	Trp	Ile	Ile	Pro	Val	Phe	Asp	Gln	Met	Tyr	Glu	
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Glu	Gln	Ile	Asn	Glu	Lys	Val	Leu	Trp	Thr	Pro	Ser	Lys	Val	Ile	Ala	
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Tyr	Lys	Asn	Arg	Ile	Pro	Val	Phe	Cys	Pro	Gly	Leu	Thr	Asp	Gly	Ser	
230				235				240								
ctt	ggg	gac	atg	cta	tac	ttc	cat	tct	ttc	aaa	aag	ggg	gat	cca	gat	824
Leu	Gly	Asp	Met	Leu	Tyr	Phe	His	Ser	Phe	Lys	Lys	Gly	Asp	Pro	Asp	
245				250				255								
aat	cca	gat	ctt	aat	cct	ggg	cta	gtc	ata	gac	att	gta	gga	gat	att	872
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agg	gcc	atg	aat	ggg	gaa	gct	gtc	cat	gct	ggg	ttg	agg	aag	aca	gga	920
Arg	Ala	Met	Asn	Gly	Glu	Ala	Val	His	Ala	Gly	Leu	Arg	Lys	Thr	Gly	
275				280				285								
atg	att	ata	ctg	ggg	gga	ggg	ctg	cct	aag	cac	cat	ggt	tgc	aat	gcc	968
Met	Ile	Ile	Leu	Gly	Gly	Gly	Leu	Pro	Lys	His	His	Val	Cys	Asn	Ala	
290				295				300								
aat	atg	atg	cgc	aat	ggg	gca	gat	ttt	gcc	gtc	ttc	att	aac	acc	gca	1016
Asn	Met	Met	Arg	Asn	Gly	Ala	Asp	Phe	Ala	Val	Phe	Ile	Asn	Thr	Ala	
310				315				320								
caa	gag	ttt	gat	ggg	agt	gac	tct	ggg	gcc	cgt	cct	gat	gaa	gct	gta	1064
Gln	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Gly	Ala	Arg	Pro	Asp	Glu	Ala	Val	
325				330				335								

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 Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val  
 370 375 380

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 gaggttggtg ataactgact agtcctctta ccatatagat aatgtatcct tgtactatga 1506  
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 <213> Lycopersicon sp.

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 <223> DHS

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 35 40 45  
 Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala  
 50 55 60  
 Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr  
 65 70 75 80  
 Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val  
 85 90 95  
 Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly  
 100 105 110  
 Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val  
 115 120 125  
 Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu  
 130 135 140  
 Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg  
 145 150 155 160  
 Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn  
 165 170 175  
 Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr  
 180 185 190  
 Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile  
 195 200 205

Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp  
 210 215 220  
 Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly  
 225 230 235 240  
 Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro  
 245 250 255  
 Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp  
 260 265 270  
 Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr  
 275 280 285  
 Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn  
 290 295 300  
 Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr  
 305 310 315 320  
 Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala  
 325 330 335  
 Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His  
 340 345 350  
 Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala  
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24

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34

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      Met Glu Asp Asp Arg Val Phe Ser Ser Val His Ser Thr Val
            1                5                10

ttc aaa gaa tcc gaa tca ttg gaa gga aag tgt gat aaa atc gaa gga      157
Phe Lys Glu Ser Glu Ser Leu Glu Gly Lys Cys Asp Lys Ile Glu Gly
      15                20                25                30

tac gat ttc aat caa gga gta gat tac cca aag ctt atg cga tcc atg      205
Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met
            35                40                45

ctc acc acc gga ttt caa gcc tcg aat ctc ggc gaa gct att gat gtc      253
Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val
            50                55                60

gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaa attccttctt      305
Val Asn Gln Met
            65

tttgttttcc tttgttttgg gtgaattagt aatgacaaag ag ttt gaa ttt gta      359
                        Phe Glu Phe Val
                                70

ttg aag cta gat tgg aga ctg gct gat gaa act aca gta gct gaa gac      407
Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu Thr Thr Val Ala Glu Asp
            75                80                85

tgt agt gaa gag gag aag aat cca tcg ttt aga gag tct gtc aag tgt      455
Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys
            90                95                100

aaa atc ttt cta ggt ttc act tca aat ctt gtt tca tct ggt gtt aga      503
Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg
            105                110                115

gat act att cgt tat ctt gtt cag cat cat atg gtttgtgatt tttgctttat      556
Asp Thr Ile Arg Tyr Leu Val Gln His His Met
            120                125

caccctgctt ttttatagat gttaaaattt tcgagcttta gttttgattt caatggtttt      616

tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat      665
      Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp
            130                135                140

ctc ata aaa tgc ctt gca cct aca ttt aaa ggt gat ttc tct cta cct      713
Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro
            145                150                155

gga gct tat tta agg tca aag gga ttg aac cga att ggg aat ttg ctg      761
Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu
            160                165                170                175

gtt cct aat gat aac tac tgc aag ttt gag gat tgg atc att ccc atc      809
Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile
            180                185                190

ttt gac gag atg ttg aag gaa cag aaa gaa gag gtattgcttt atctttcctt      862
Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu
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[illegible]

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 <212> PRT  
 <213> Arabidopsis sp.

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 35 40 45  
 Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val Val Asn  
 50 55 60  
 Gln Met Phe Glu Phe Val Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu  
 65 70 75 80  
 Thr Thr Val Ala Glu Asp Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe  
 85 90 95  
 Arg Glu Ser Val Lys Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu  
 100 105 110  
 Val Ser Ser Gly Val Arg Asp Thr Ile Arg Tyr Leu Val Gln His His  
 115 120 125  
 Met Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp Leu  
 130 135 140  
 Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro Gly  
 145 150 155 160  
 Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val  
 165 170 175  
 Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Phe  
 180 185 190  
 Asp Glu Met Leu Lys Glu Gln Lys Glu Glu Asn Val Leu Trp Thr Pro  
 195 200 205  
 Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu Ile Asn Asn Glu Ser Ser  
 210 215 220  
 Tyr Leu Tyr Trp Ala Tyr Lys Met Asn Ile Pro Val Phe Cys Pro Gly  
 225 230 235 240  
 Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg  
 245 250 255  
 Thr Ser Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala Met Asn  
 260 265 270  
 Gly Glu Ala Val His Ala Asn Pro Lys Lys Thr Gly Met Ile Ile Leu  
 275 280 285

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Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg  
 290 295 300

Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Gly Gln Glu Phe Asp  
 305 310 315 320

Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys  
 325 330 335

Ile Arg Gly Ser Ala Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser  
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His Pro Asn Leu Tyr Leu Thr Gln Trp Phe  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

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<210> 8  
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<220>  
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 attgaactac tgcaattcta aaactttggt tacattttta ttccatcaaa gattgagttc 240  
 agcataggaa aaagg atg gag gat gct aat cat gat agt gtg gca tct gcg 291  
 Met Glu Asp Ala Asn His Asp Ser Val Ala Ser Ala  
 1 5 10  
 cac tct gca gca ttc aaa aag tcg gag aat tta gag ggg aaa agc gtt 339  
 His Ser Ala Ala Phe Lys Lys Ser Glu Asn Leu Glu Gly Lys Ser Val



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gcc att gaa gta gtt aat cat atg cta gat tgg agt ctg gca gat gag Ala Ile Glu Val Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu 65 70 75			483
gca cct gtg gac gat tgt agc gag gaa gag agg gat cct aaa ttc aga Ala Pro Val Asp Asp Cys Ser Glu Glu Arg Asp Pro Lys Phe Arg 80 85 90			531
gaa tct gtg aag tgc aaa gtg ttc ttg ggc ttt act tca aat ctt att Glu Ser Val Lys Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile 95 100 105			579
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gtt gac gtg ata gta acg aca acc gga ggt ata gaa gaa gat cta ata Val Asp Val Ile Val Thr Thr Gly Gly Ile Glu Glu Asp Leu Ile 125 130 135 140			675
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gcc tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt Ala Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly 160 165 170			771
aat ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile 175 180 185			819
att cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc Ile Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile 190 195 200			867
tta tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac Leu Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn 205 210 215 220			915
gat gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta Asp Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val 225 230 235			963
ttt tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe 240 245 250			1011
cat tct ttt cgc aat ccg ggt tta atc gtc gat gtt gtg caa gat ata His Ser Phe Arg Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile 255 260 265			1059
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atg att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca 1155
Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala
285 290 295 300

aac atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac act gcc 1203
Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala
305 310 315

gaa gag ttt gac ggc agt gat tct ggt gct cgc ccc gat gag gct att 1251
Glu Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile
320 325 330

tca tgg ggc aaa att agc gga tct gct aag act gtg aag gtg cat tgt 1299
Ser Trp Gly Lys Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys
335 340 345

gat gcc acg ata gct ttc cct cta cta gtc gct gag aca ttt gca gca 1347
Asp Ala Thr Ile Ala Phe Pro Leu Leu Val Ala Glu Thr Phe Ala Ala
350 355 360

aaa aga gaa aaa gag agg aag agc tgt taaaactttt ttgattgttg 1394
Lys Arg Glu Lys Glu Arg Lys Ser Cys
365 370

aaaaatctgt gttatacaag tctcgaaatg catttttagta attgacttga tcttatcatt 1454

tcaatgtggt atctttgaaa atgttggttaa tgaaacatct cacctcttct atacaacatt 1514

gttgatccat tgtactccgt atcttgtaat tttggaaaaa aaaaaccgtc tattgttacg 1574

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<213> Dianthus sp.

<220>
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35 40 45

Ala Ser Asn Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Glu Val
50 55 60

Val Asn His Met Leu Asp Trp Ser Leu Ala Asp Glu Ala Pro Val Asp
65 70 75 80

Asp Cys Ser Glu Glu Glu Arg Asp Pro Lys Phe Arg Glu Ser Val Lys
85 90 95

Cys Lys Val Phe Leu Gly Phe Thr Ser Asn Leu Ile Ser Ser Gly Val
100 105 110

Arg Asp Thr Ile Arg Tyr Leu Val Gln His His Met Val Asp Val Ile

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Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu Pro Gly		
145	150	155
Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val		
165	170	175
Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile Leu		
180	185	190
Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp Thr Pro		
195	200	205
Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu Ser Ser		
210	215	220
Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys Pro Gly		
225	230	235
Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Arg		
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Asn Pro Gly Leu Ile Val Asp Val Val Gln Asp Ile Arg Ala Val Asn		
260	265	270
Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile Ile Leu		
275	280	285
Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met Met Arg		
290	295	300
Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr Ala Glu Glu Phe Asp		
305	310	315
Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Ile Ser Trp Gly Lys		
325	330	335
Ile Ser Gly Ser Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile		
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5 10 15 20

cca cag caa gct gga acc atc cgt aag aat ggt tac atc gtt atc aaa 150
Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val Ile Lys
25 30 35

ggc cgt ccc tgc aag gtt gtt gag gtc tcc act tca aaa act gga aaa 198
Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr Gly Lys
40 45 50

cac gga cat gct aaa tgt cac ttt gtg gca att gac att ttc aat gga 246
His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe Asn Gly
55 60 65

aag aaa ctg gaa gat atc gtt ccg tcc tcc cac aat tgt gat gtg cca 294
Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp Val Pro
70 75 80

cat gtt aac cgt acc gac tat cag ctg att gat atc tct gaa gat ggt 342
His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu Asp Gly
85 90 95 100

ttt gtc tca ctt ctt act gaa agt gga aac acc aag gat gac ctc agg 390
Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys Asp Asp Leu Arg
105 110 115

ctt ccc acc gat gaa aat ctg ctg aag cag gtt aaa gat ggg ttc cag 438
Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys Asp Gly Phe Gln
120 125 130

gaa gga aag gat ctt gtg gtg tct gtt atg tct gcg atg ggc gaa gag 486
Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly Glu Glu
135 140 145

cag att aac gcc gtt aag gat gtt ggt acc aag aat tagttatgtc 532
Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn
150 155 160

atggcagcat aatcactgcc aaagcttttaa gacattatca tatectaatag tgggtactttg 592

atatcactag attataaact gtgttattttg cactgttcaa aacaaaagaa agaaaactgc 652

tgttatggct agagaaagta ttggctttga gcttttgaca gcacagttga actatgtgaa 712

aattctactt tttttttttt gggtaaaata ctgctcgttt aatgttttgc aaaaaaaaaa 772

aaaaaaaaa 780

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<210> 12  
 <211> 160  
 <212> PRT  
 <213> Lycopersicon sp.

<220>  
 <223> eif-5A

<400> 12  
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 1 5 10 15  
 Ser Lys Thr Phe Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr

	20		25		30
Ile Val	Ile Lys Gly Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser				
	35		40		45
Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp					
	50		55		60
Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn					
	65		70		75
Cys Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile					
		85		90	95
Ser Glu Asp Gly Phe Val Ser Leu Leu Thr Glu Ser Gly Asn Thr Lys					
	100		105		110
Asp Asp Leu Arg Leu Pro Thr Asp Glu Asn Leu Leu Lys Gln Val Lys					
	115		120		125
Asp Gly Phe Gln Glu Gly Lys Asp Leu Val Val Ser Val Met Ser Ala					
	130		135		140
Met Gly Glu Glu Gln Ile Asn Ala Val Lys Asp Val Gly Thr Lys Asn					
	145		150		155
					160

<210> 13  
 <211> 812  
 <212> DNA  
 <213> Dianthus sp.

<220>  
 <223> eif-5A

<220>  
 <221> CDS  
 <222> (67)..(546)

<400> 13  
 ctctttttaca tcaatcgaaa aaaaattagg gttctttattt tagagtgaga ggcgaaaaat 60

cgaacg atg tcg gac gac gat cac cat ttc gag tca tcg gcc gac gcc	108
Met Ser Asp Asp Asp His His Phe Glu Ser Ser Ala Asp Ala	
1 5 10	
gga gca tcc aag act tac cct caa caa gct ggt aca atc cgc aag agc	156
Gly Ala Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser	
15 20 25 30	
ggt cac atc gtc atc aaa aat cgc cct tgc aag gtg gtt gag gtt tct	204
Gly His Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser	
35 40 45	
acc tcc aag act ggc aag cac ggt cat gcc aaa tgt cac ttt gtt gcc	252
Thr Ser Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala	
50 55 60	
att gac att ttc aac ggc aag aag ctg gaa gat att gtc ccc tca tcc	300
Ile Asp Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser	
65 70 75	
cac aat tgt gat gtt cca cat gtc aac cgt gtc gac tac cag ctg ctt	348
His Asn Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu	
80 85 90	

gat atc act gaa gat ggc ttt gtt agt ctg ctg act gac agt ggt gac 396  
 Asp Ile Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp  
 95 100 105 110

acc aag gat gat ctg aag ctt cct gct gat gag gcc ctt gtg aag cag 444  
 Thr Lys Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln  
 115 120 125

atg aag gag gga ttt gag gcg ggg aaa gac ttg att ctg tca gtc atg 492  
 Met Lys Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met  
 130 135 140

tgt gca atg gga gaa gag cag atc tgc gcc gtc aag gac gtt agt ggt 540  
 Cys Ala Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly  
 145 150 155

ggc aag tagaagcttt tgatgaatcc aatactacgc ggtgcagttg aagcaatagt 596  
 Gly Lys  
 160

aatctcgaga acattctgaa ccttatatgt tgaattgatg gtgcttagtt tgttttggaa 656

atctcttttgc aattaagttg taccaaataca atggatgtaa tgtcttgaat ttgttttatt 716

tttgttttga tgtttgtctgt gattgcatta tgcattgtta tgagttatga cctgttataa 776

cacaaggttt tggtaaaaaa aaaaaaaaaa aaaaaa 812

<210> 14  
 <211> 160  
 <212> PRT  
 <213> Dianthus sp.

<220>  
 <223> eif-5A

<400> 14  
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 1 5 10 15  
 Ser Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Ser Gly His  
 20 25 30  
 Ile Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser  
 35 40 45  
 Lys Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp  
 50 55 60  
 Ile Phe Asn Gly Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn  
 65 70 75 80  
 Cys Asp Val Pro His Val Asn Arg Val Asp Tyr Gln Leu Leu Asp Ile  
 85 90 95  
 Thr Glu Asp Gly Phe Val Ser Leu Leu Thr Asp Ser Gly Asp Thr Lys  
 100 105 110  
 Asp Asp Leu Lys Leu Pro Ala Asp Glu Ala Leu Val Lys Gln Met Lys  
 115 120 125  
 Glu Gly Phe Glu Ala Gly Lys Asp Leu Ile Leu Ser Val Met Cys Ala  
 130 135 140  
 Met Gly Glu Glu Gln Ile Cys Ala Val Lys Asp Val Ser Gly Gly Lys

145

150

155

160

<210> 15  
 <211> 702  
 <212> DNA  
 <213> Arabidopsis sp.

<220>  
 <223> eif-5A

<220>  
 <221> CDS  
 <222> (56)..(529)

<400> 15  
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 Met  
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tcc gac gag gag cat cac ttt gag tcc agt gac gcc gga gcg tcc aaa 106  
 Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser Lys  
 5 10 15

acc tac cct caa caa gct gga acc atc cgt aag aat ggt tac atc gtc 154  
 Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile Val  
 20 25 30

atc aaa aat cgt ccc tgc aag gtt gtt gag gtt tca acc tcg aag act 202  
 Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys Thr  
 35 40 45

ggc aag cat ggt cat gct aaa tgt cat ttt gta gct att gat atc ttc 250  
 Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile Phe  
 50 55 60 65

acc agc aag aaa ctc gaa gat att gtt cct tct tcc cac aat tgt gat 298  
 Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys Asp  
 70 75 80

gtt cct cat gtc aac cgt act gat tat cag ctg att gac att tct gaa 346  
 Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser Glu  
 85 90 95

gat gga tat gtc agt ttg ttg act gat aac ggt agt acc aag gat gac 394  
 Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp Asp  
 100 105 110

ctt aag ctc cct aat gat gac act ctg ctc caa cag atc aag agt ggg 442  
 Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser Gly  
 115 120 125

ttt gat gat gga aaa gat cta gtg gtg agt gta atg tca gct atg gga 490  
 Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met Gly  
 130 135 140 145

gag gaa cag atc aat gct ctt aag gac atc ggt ccc aag tgagactaac 539  
 Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys  
 150 155

aaagcctccc ctttgttatg agattcttct tcttctgtag gcttccatta ctcgtcggag 599

attatcttgt ttttgggtta ctccattttt ggatatttaa acttttgtta ataatgccat 659

cttcttcaac cttttccttc tagatggttt ttatacttct tct 702

<210> 16  
 <211> 158  
 <212> PRT  
 <213> Arabidopsis sp.

<220>  
 <223> eif-5A

<400> 16  
 Met Ser Asp Glu Glu His His Phe Glu Ser Ser Asp Ala Gly Ala Ser  
 1 5 10 15  
 Lys Thr Tyr Pro Gln Gln Ala Gly Thr Ile Arg Lys Asn Gly Tyr Ile  
 20 25 30  
 Val Ile Lys Asn Arg Pro Cys Lys Val Val Glu Val Ser Thr Ser Lys  
 35 40 45  
 Thr Gly Lys His Gly His Ala Lys Cys His Phe Val Ala Ile Asp Ile  
 50 55 60  
 Phe Thr Ser Lys Lys Leu Glu Asp Ile Val Pro Ser Ser His Asn Cys  
 65 70 75 80  
 Asp Val Pro His Val Asn Arg Thr Asp Tyr Gln Leu Ile Asp Ile Ser  
 85 90 95  
 Glu Asp Gly Tyr Val Ser Leu Leu Thr Asp Asn Gly Ser Thr Lys Asp  
 100 105 110  
 Asp Leu Lys Leu Pro Asn Asp Asp Thr Leu Leu Gln Gln Ile Lys Ser  
 115 120 125  
 Gly Phe Asp Asp Gly Lys Asp Leu Val Val Ser Val Met Ser Ala Met  
 130 135 140  
 Gly Glu Glu Gln Ile Asn Ala Leu Lys Asp Ile Gly Pro Lys  
 145 150 155

<210> 17  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 17  
 aaarrycgmc cytgcaaggt

20

<210> 18  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 18  
 aatacgactc actatag

17



<210> 19  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<220>  
 <223> "n" bases represent a, t, c, g, other or unknown

<400> 19  
 tcyttncct cmkctaahcc 20

<210> 20  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 20  
 attaaccctc actaaag 17

<210> 21  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 21  
 ctgttaccaa aaaatctgta cc 22

<210> 22  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 22  
 agaagaagta taaaaacccat c 21

<210> 23  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 23  
 aaagaatcct agagagagaa agg 23

<210> 24  
 <211> 18  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 24

ttttacatca atcgaaaa

18

<210> 25

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

accaaaacct gtgttataac tcc

23

<210> 26

<211> 581

<212> DNA

<213> Arabidopsis sp.

<220>

<223> DHS

<220>

<221> CDS

<222> (1)..(579)

<400> 26

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Gly	Gly	Val	Glu	Glu	Asp	Leu	Ile	Lys	Cys	Leu	Ala	Pro	Thr	Phe	Lys	
1				5					10					15		

ggt	gat	ttc	tct	cta	cct	gga	gct	tat	tta	agg	tca	aag	gga	ttg	aac	96
Gly	Asp	Phe	Ser	Leu	Pro	Gly	Ala	Tyr	Leu	Arg	Ser	Lys	Gly	Leu	Asn	
			20					25					30			

cga	att	ggg	aat	ttg	ctg	ggt	cct	aat	gat	aac	tac	tgc	aag	ttt	gag	144
Arg	Ile	Gly	Asn	Leu	Leu	Val	Pro	Asn	Asp	Asn	Tyr	Cys	Lys	Phe	Glu	
		35					40					45				

gat	tgg	atc	att	ccc	atc	ttt	gac	gag	atg	ttg	aag	gaa	cag	aaa	gaa	192
Asp	Trp	Ile	Ile	Pro	Ile	Phe	Asp	Glu	Met	Leu	Lys	Glu	Gln	Lys	Glu	
	50					55					60					

gag	aat	gtg	ttg	tgg	act	cct	tct	aaa	ctg	tta	gca	cgg	ctg	gga	aaa	240
Glu	Asn	Val	Leu	Trp	Thr	Pro	Ser	Lys	Leu	Leu	Ala	Arg	Leu	Gly	Lys	
65					70				75					80		

gaa	atc	aac	aat	gag	agt	tca	tac	ctt	tat	tgg	gca	tac	aag	atg	aat	288
Glu	Ile	Asn	Asn	Glu	Ser	Ser	Tyr	Leu	Tyr	Trp	Ala	Tyr	Lys	Met	Asn	
			85					90						95		

att	cca	gta	ttc	tgc	cca	ggg	tta	aca	gat	ggc	tct	ctt	agg	gat	atg	336
Ile	Pro	Val	Phe	Cys	Pro	Gly	Leu	Thr	Asp	Gly	Ser	Leu	Arg	Asp	Met	
			100				105						110			

ctg	tat	ttt	cac	tct	ttt	cgt	acc	tct	ggc	ctc	atc	atc	gat	gta	gta	384
Leu	Tyr	Phe	His	Ser	Phe	Arg	Thr	Ser	Gly	Leu	Ile	Ile	Asp	Val	Val	
		115				120						125				

caa gat atc aga gct atg aac ggc gaa gct gtc cat gca aat cct aaa	432
Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys	
130 135 140	
aag aca ggg atg ata atc ctt gga ggg ggc ttg cca aag cac cac ata	480
Lys Thr Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile	
145 150 155 160	
tgt aat gcc aat atg atg cgc aat ggt gca gat tac gct gta ttt ata	528
Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile	
165 170 175	
aac acc ggg caa gaa ttt gat ggg agc gac tcg ggt gca cgc cct gat	576
Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp	
180 185 190	
gaa gc	581
Glu	
<210> 27	
<211> 522	
<212> DNA	
<213> Dianthus sp.	
<220>	
<223> DHS	
<220>	
<221> CDS	
<222> (3)..(521)	
<400> 27	
ga aga tcc atc aag tgc ctt gca ccc act ttc aaa ggc gat ttt gcc	47
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala	
1 5 10 15	
tta cca gga gct caa tta cgc tcc aaa ggg ttg aat cga att ggt aat	95
Leu Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn	
20 25 30	
ctg ttg gtt ccg aat gat aac tac tgt aaa ttt gag gat tgg atc att	143
Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile	
35 40 45	
cca att tta gat aag atg ttg gaa gag caa att tca gag aaa atc tta	191
Pro Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu	
50 55 60	
tgg aca cca tcg aag ttg att ggt cga tta gga aga gaa ata aac gat	239
Trp Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp	
65 70 75	
gag agt tca tac ctt tac tgg gcc ttc aag aac aat att cca gta ttt	287
Glu Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe	
80 85 90 95	
tgc cca ggt tta aca gac ggc tca ctc gga gac atg cta tat ttt cat	335
Cys Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His	
100 105 110	
tct ttt cgc aat ccg ggt tta atc atc gat gtt gtg caa gat ata aga	383
Ser Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg	
115 120 125	
gca gta aat ggc gag gct gtg cac gca gcg cct agg aaa aca ggc atg	431

Ala Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met  
130 135 140

att ata ctc ggt gga ggg ttg cct aag cac cac atc tgc aac gca aac 479  
Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn  
145 150 155

atg atg aga aat ggc gcc gat tat gct gtt ttc atc aac acc g 522  
Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr  
160 165 170

<210> 28  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 28  
ttgargaaga tycatmaat gcct 24

<210> 29  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 29  
ccatcaaayt cytgkgcrgt gtt 23

<210> 30  
<211> 484  
<212> DNA  
<213> Arabidopsis sp.

<220>  
<223> DHS

<220>  
<221> CDS  
<222> (2)..(112)

<400> 30  
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Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala  
1 5 10 15

aaa acc gtt aag gtc tgc ttt tta att tct tca cat cct aat tta tat 97  
Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr  
20 25 30

ctc act cag tgg ttt tgagtacata tttaatattg gatcattcct gcagggtatac 152  
Leu Thr Gln Trp Phe  
35

tgtgatgcta ccatagcctt occattgttg gttgcagaaa catttgccac aaagagagac 212  
caaacctgtg agtctaagac ttaagaactg actggctcgtt ttggccatgg attcttaaag 272  
atcggttgctt tttgatttta cactggagtg accatataac actccacatt gatgtggctg 332

tgaacggaat tgtttttttg cgaattgtac tttagttttct ctcaacctaa aatgatttgc 392  
 agattgtggt ttogttttaa acacaagagt cttgtagtca ataattccttt gccttataaa 452  
 attattcagt tccaacaaaa aaaaaaaaaa aa 484

<210> 31  
 <211> 559  
 <212> DNA  
 <213> Lycopersicon sp.

<220>  
 <223> DHS

<220>  
 <221> CDS  
 <222> (1)..(156)

<220>  
 <223> "n" bases represent a, t, c, g, other or unknown

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 Gly Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Gly  
 1 5 10 15  
 gcc aag act gtg aag gtg cat tgt gat gca acc att gca ttt ccc ata 96  
 Ala Lys Thr Val Lys Val His Cys Asp Ala Thr Ile Ala Phe Pro Ile  
 20 25 30  
 tta gta gct gag aca ttt gca gct aag agt aag gaa ttc tcc cag ata 144  
 Leu Val Ala Glu Thr Phe Ala Ala Lys Ser Lys Glu Phe Ser Gln Ile  
 35 40 45  
 agg tgc caa gtt tgaacattga ggaagctgtc cttccgacca cacatatgaa 196  
 Arg Cys Gln Val  
 50  
 ttgctagctt ttgaagccaa cttgctagtg tgcagcacca tttattctgc aaaactgact 256  
 agagagcagg gtatattcct ctaccccgag ttagacgaca tcctgtatgg ttcaaattaa 316  
 ttattttttct ccccttcaca ccatgttatt tagtttctctt cctcttcgaa agtgaagagc 376  
 ttagatgttc ataggttttg aattatgttg gaggttggtg ataactgact agtcctctta 436  
 ccatatagat aatgtatcct tgtactatga gattttgggt gtgtttgata ccaaggaaaa 496  
 atgtttatatt ggaaaacaat tggattttta atttaaaaaa aattgnttaa aaaaaaaaaa 556  
 aaa 559

<210> 32  
 <211> 193  
 <212> PRT  
 <213> Arabidopsis sp.

<220>  
 <223> DHS

<400> 32  
 Gly Gly Val Glu Glu Asp Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys  
 1 5 10 15

006277 6T052260

Gly Asp Phe Ser Leu Pro Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn  
20 25 30  
Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu  
35 40 45  
Asp Trp Ile Ile Pro Ile Phe Asp Glu Met Leu Lys Glu Gln Lys Glu  
50 55 60  
Glu Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys  
65 70 75 80  
Glu Ile Asn Asn Glu Ser Ser Tyr Leu Tyr Trp Ala Tyr Lys Met Asn  
85 90 95  
Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser Leu Arg Asp Met  
100 105 110  
Leu Tyr Phe His Ser Phe Arg Thr Ser Gly Leu Ile Ile Asp Val Val  
115 120 125  
Gln Asp Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Asn Pro Lys  
130 135 140  
Lys Thr Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Ile  
145 150 155 160  
Cys Asn Ala Asn Met Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile  
165 170 175  
Asn Thr Gly Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp  
180 185 190  
Glu

<210> 33  
<211> 173  
<212> PRT  
<213> Dianthus sp.

<220>  
<223> DHS

<400> 33  
Arg Ser Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ala Leu  
1 5 10 15  
Pro Gly Ala Gln Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu  
20 25 30  
Leu Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro  
35 40 45  
Ile Leu Asp Lys Met Leu Glu Glu Gln Ile Ser Glu Lys Ile Leu Trp  
50 55 60  
Thr Pro Ser Lys Leu Ile Gly Arg Leu Gly Arg Glu Ile Asn Asp Glu  
65 70 75 80  
Ser Ser Tyr Leu Tyr Trp Ala Phe Lys Asn Asn Ile Pro Val Phe Cys  
85 90 95  
Pro Gly Leu Thr Asp Gly Ser Leu Gly Asp Met Leu Tyr Phe His Ser  
100 105 110

Phe Arg Asn Pro Gly Leu Ile Ile Asp Val Val Gln Asp Ile Arg Ala  
115 120 125

Val Asn Gly Glu Ala Val His Ala Ala Pro Arg Lys Thr Gly Met Ile  
130 135 140

Ile Leu Gly Gly Gly Leu Pro Lys His His Ile Cys Asn Ala Asn Met  
145 150 155 160

Met Arg Asn Gly Ala Asp Tyr Ala Val Phe Ile Asn Thr  
165 170

<210> 34  
<211> 37  
<212> PRT  
<213> Arabidopsis sp.

<220>  
<223> DHS

<400> 34  
Ala Arg Pro Asp Glu Ala Val Ser Trp Gly Lys Ile Arg Gly Ser Ala  
1 5 10 15

Lys Thr Val Lys Val Cys Phe Leu Ile Ser Ser His Pro Asn Leu Tyr  
20 25 30

Leu Thr Gln Trp Phe  
35

<210> 35  
<211> 52  
<212> PRT  
<213> Lycopersicon sp.

<220>  
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Arg Cys Gln Val  
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